Figure 1

bcl Consensus PCR Primers

```
                                    Ile
EcoRI AspTrpGlyArgValValAla
5- AGATCTGAATTCAACTTGGGGGIC(A)GIA(G)TXGTXGC -3' bclx 1-32


          AspTrpGlyGlyGlnGluAsnAspGlnIleTrp
                  AGGGTIGGIGGXACXAGA(G)ACA(T)(C)TAGGT
5'- AGATCT'AAGCTTGTCCCAICCICCXTGXTCC(T)TGA(G)ATCCA -3' bclX 2-39
```

Figure 2

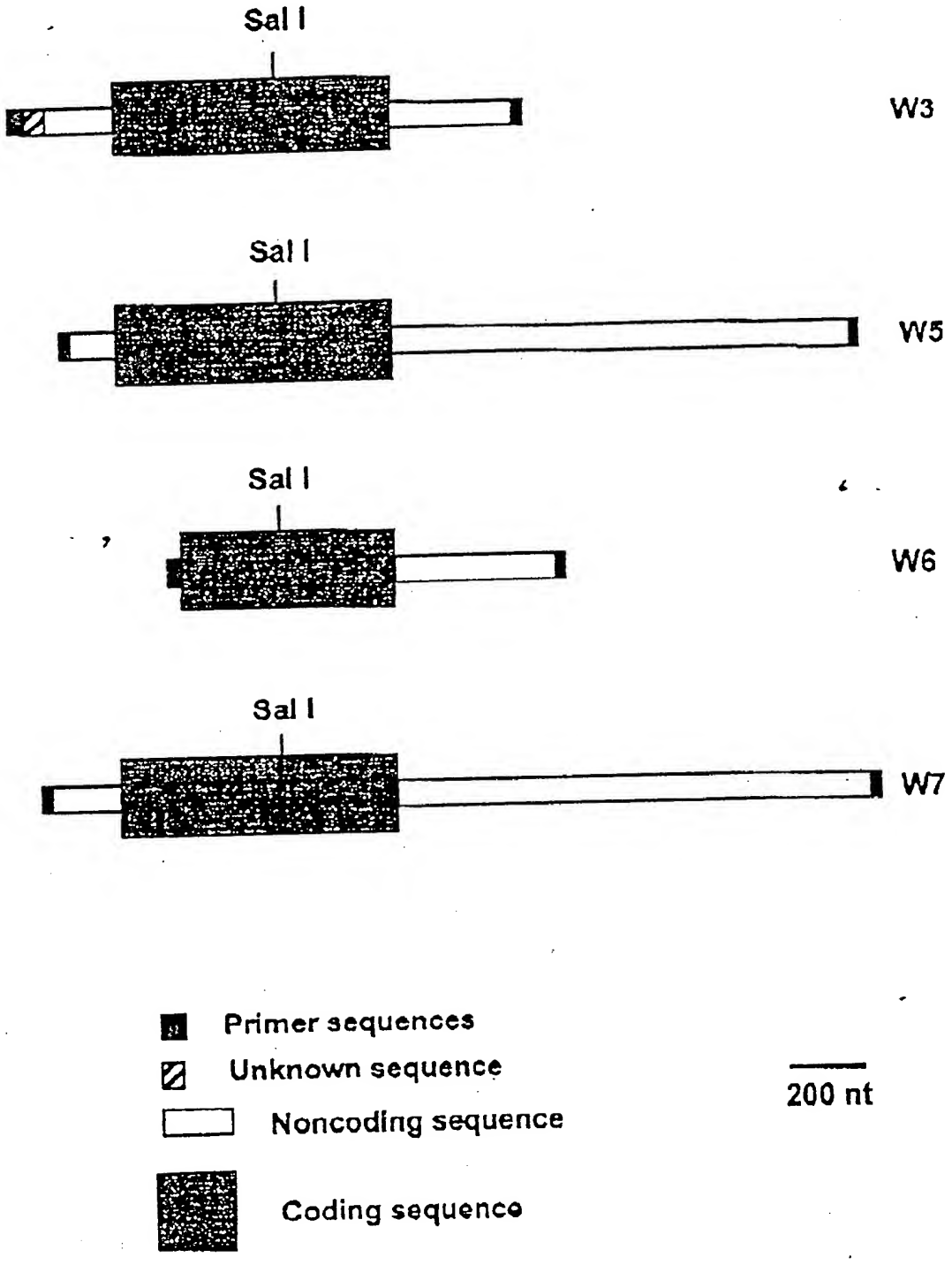

Cdi-1 cDNA clones
Sal I
W3
Sal I
W5
Sal I
W6
Sal I
W7
Primer sequences
Unknown sequence
Noncoding sequence
Coding sequence
200 nt

Figure 3

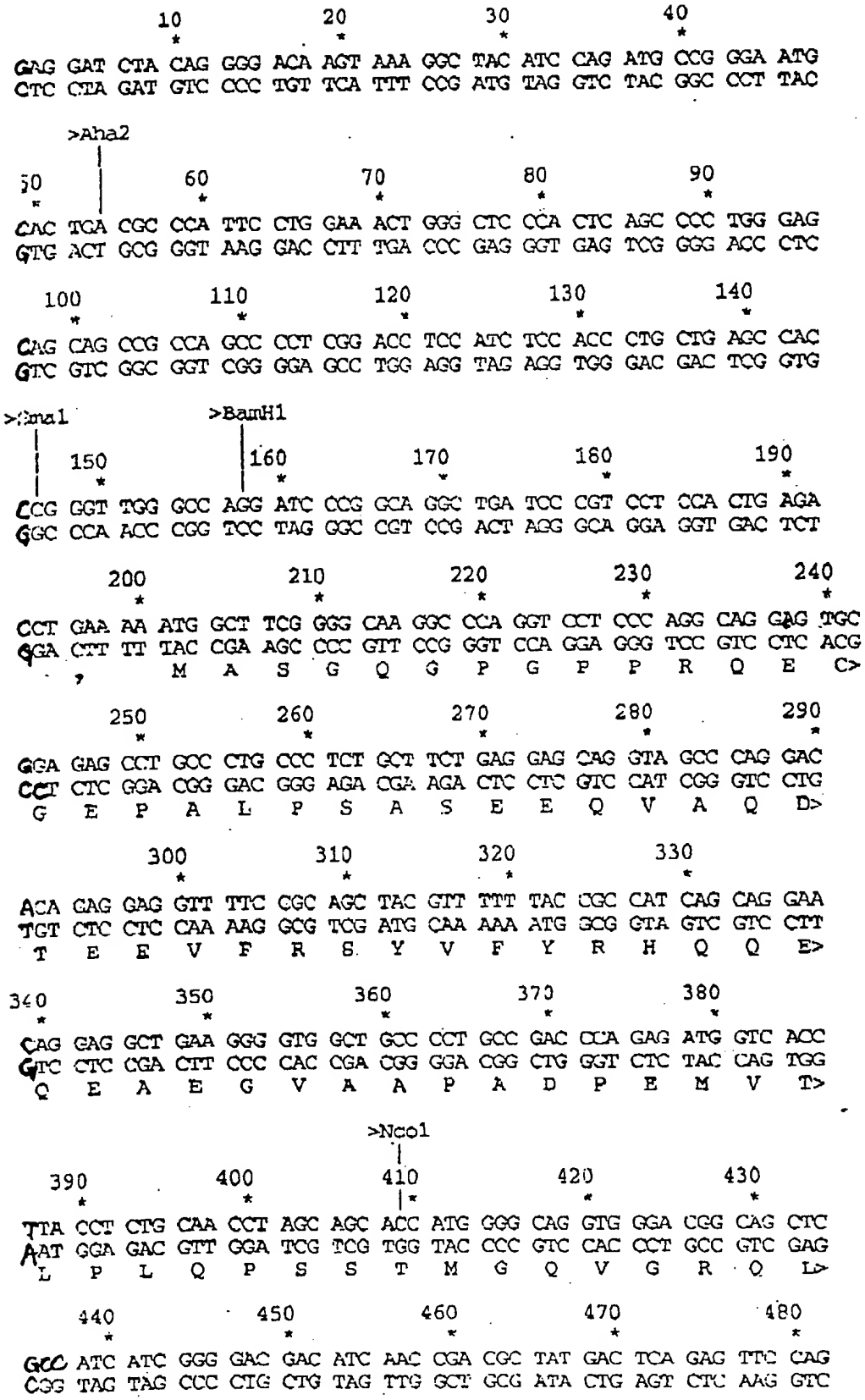


Figure 3 cont.

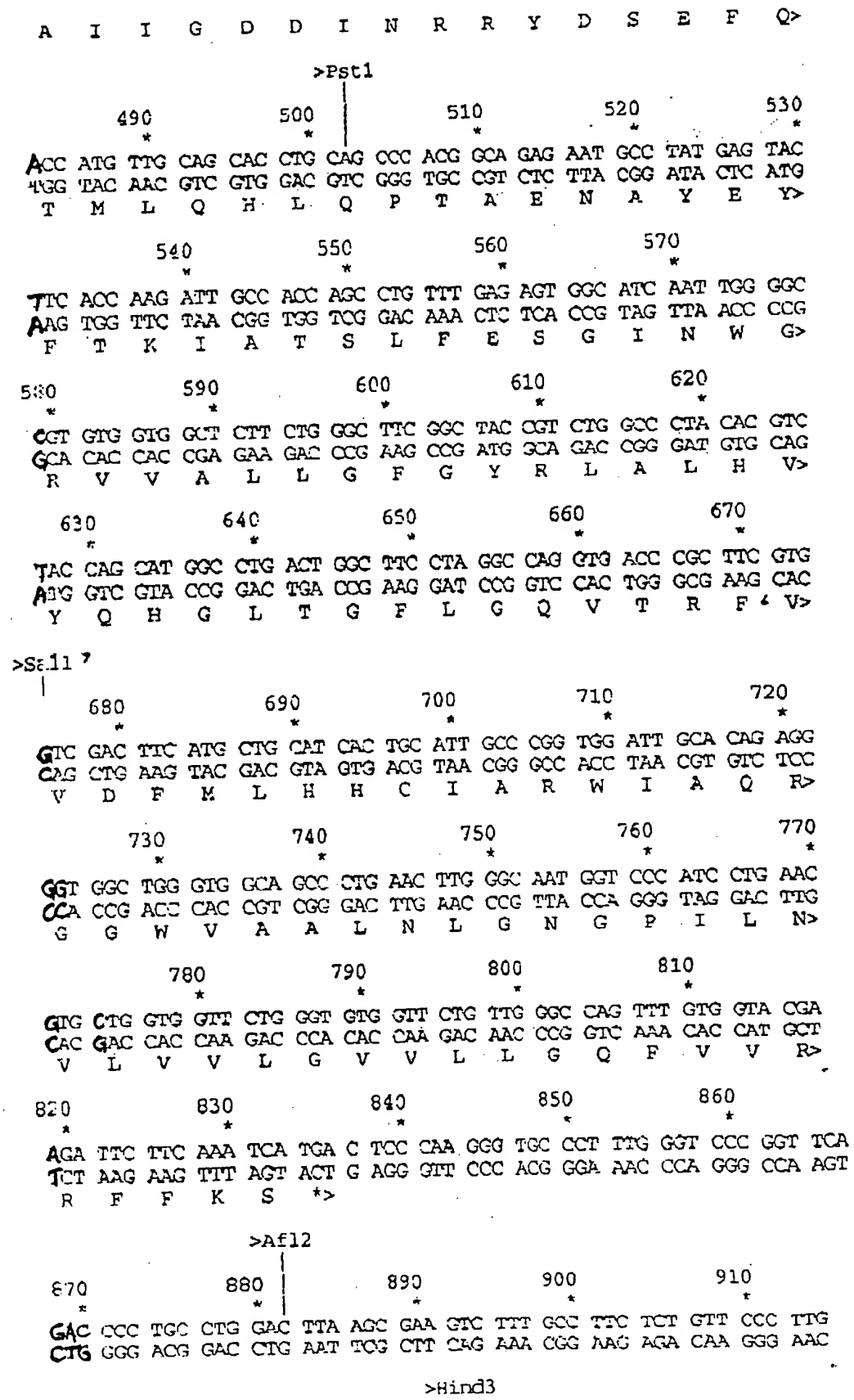


Figure 3 cont.

```
    920         930         940         950         960
     *           *           *           *           *
CAG GGT CCC CCC TCA AGA GTA CAG AAG CTT TAG CAA GTG TGC ACT CCA
GTC CCA GGG GGG AGT TCT CAT GTC TTC GAA ATC GTT CAC ACG TGA GGT

                                        >Pst1
                                          |
       970         980         990        1000        1010
        *           *           *           *           *
GCT TCG GAG GCC CTG CGT GGG GGC CAG TCA GGC TGC AGA GGC ACC TCA
CGA AGC CTC CGG GAC GCA CCC CCG GTC AGT CCG ACG TCT CCG TGG AGT

                                    >Apa1
                                      |
         1020        1030        1040 |      1050
           *           *           *  |        *
ACA TTG CAT GGT GCT AGT GCC CTC TCT CTG GGC CCA GGG CTG TGG CCG
TGT AAC GTA CCA CGA TCA CGG GAG AGA GAC CCG GGT CCC GAC ACC GGC

1060     1070        1080        1090        1100
 *         *           *           *           *
TCT CCT CCC TCA GCT CTC TGG GAC CTC CTT AGC CCT GTC TGC TAG GCG
AGA GGA GGG AGT CGA GAG ACC CTG GAG GAA TCG GGA CAG ACG ATC CGC

1110        1120        1130        1140        1150
 *           *           *           *           *
CTG GGG AGA CTG ATA ACT TGG GGA GGC AAG AGA CTG GGA GCC ACT TCT
GAC CCC TCT GAC TAT TGA ACC CCT CCG TTC TCT GAC CCT CGG TGA AGA

   1160        1170        1180        1190        1200
     *           *           *           *           *
CCC CAG AAA GTG TTT AAC GGT TTT AGC TTT TTA TAA TAC CCT TGT GAG
GGG GTC TTT CAC AAA TTG CCA AAA TCG AAA AAT ATT ATG GGA ACA CTC

                                    >Aha2
                                      |
      1210        1220        1230    |   1240        1250
        *           *           *     |     *           *
AGC CCA TTC CCA CCA TTC TAC CTG AGG CCA GGA CGT CTG GGG TGT GGG
TCG GGT AAG GGT GGT AAG ATG GAC TCC GGT CCT GCA GAC CCC ACA CCC

       1260        1270        1280        1290
         *           *           *           *
GAT TGG TGG GTC TAT GTT CCC CAG GAT TCA GCT ATT CTG GAA CAT CAG
CTA ACC ACC CAG ATA CAA GGG GTC CTA AGT CGA TAA GAC CTT CTA GTC

1300        1310        1320        1330        1340
 *           *           *           *           *
CAC CCT AAG AGA TGG GAC TAG GAC CTG AGC CTG GTC CTG GCC GTC CCT
GTG GGA TTC TCT ACC CTG ATC CTG GAC TCG GAC CAG GAC CGG CAG GGA

1350        1360        1370        1380        1390
 *           *           *           *           *
AAG CAT GTG TCC CAG GAG CAG GAC CTA CTA GGA GAG GGG GGC CAA GGT
TTC GTA CAC AGG GTC CTC GTC CTG GAT GAT CCT CTC CCC CCG GTT CCA

   1400        1410        1420        1430        1440
     *           *           *           *           *
CCT GCT CAA CTC TAC CCC TGC TCC CAT TCC TCC CTC CGG CCA TAC TGC
GGA CGA GTT GAG ATG GGG ACG AGG GTA AGG AGG GAG GCC GGT ATG ACG
```

Figure 3 cont.

```
    1450       1460       1470       1480       1490
      *          *          *          *          *
CTT TGC AGT TGG ACT CTC AGG GAT TCT GGG CTT GGG GTG TGG GGT GGG
GAA ACG TCA ACC TGA GAG TCC CTA AGA CCC GAA CCC CAC ACC CCA CCC

    1500       1510       1520       1530
      *          *          *          *
GTG GAG TCG CAG ACC AGA GCT GTC TGA ACT CAC GTG TCA GAA GCC TCC
CAC CTC AGC GTC TGG TCT CGA CAG ACT TGA GTG CAC AGT CTT CGG AGG

1540       1550       1560       1570       1580
*          *          *          *          *
AAG CCT GCC TCC CAA GGT CCT CTC AGT TCT CTC CCT TCC TCT CTC CTT
TTC GGA CGG AGG GTT CCA GGA GAG TCA AGA GAG GGA AGG AGA GAG GAA

1590       1600       1610       1620       1630
*          *          *          *          *
ATA GAC ACT TGC TCC CAA CCC ATT CAC TAC AGG TGA AGG CTC TCA CCC
TAT CTG TGA ACG AGG GTT GGG TAA GTG ATG TCC ACT TCC GAG AGT GGG

    1640       1650       1660       1670       1680
      *          *          *          *          *
ATC CCT GGG GGC CTT GGG TGA GTG GCC TGC TAA GGC TCC TCC TTG CCC
TAG GGA CCC CCG GAA CCC ACT CAC CGG ACG ATT CCG AGG AGG AAC GGG

      1690       1700       1710       1720       1730
        *          *          *          *          *
AGA CTA CAG GGC TTA GGA CTT GGT TTG TTA TAT CAG GGA AAA GGA GTA
TCT GAT GTC CCG AAT CCT GAA CCA AAC AAT ATA GTC CCT TTT CCT CAT

        1740       1750       1760       1770
          *          *          *          *
GGG AGT TCA TCT GGA GGG TTC TAA GTG GGA GAA GGA CTA TCA ACA CCA
CCC TCA AGT AGA CCT CCC AAG ATT CAC CCT CTT CCT GAT AGT TGT GGT

                    >BamH1
1780       1790       |1800       1810       1820
*          *          | *          *          *
CTA GGA ATC CCA GAG GTG GAT CCT CCC TCA TGG CTC TGG CAC AGT GTA
GAT CCT TAG GGT CTC CAC CTA GGA GGG AGT ACC GAG ACC GTG TCA CAT

1830       1840       1850       1860       1870
*          *          *          *          *
ATC CAG GGG TGT AGA TGG GGG AAC TGT GAA TAC TTG AAC TCT GTT CCC
TAG GTC CCC ACA TCT ACC CCC TTG ACA CTT ATG AAC TTG AGA CAA GGG

    1880       1890       1900       1910       1920
      *          *          *          *          *
CCA CCC TCC ATG CTC CTC ACC TGT CTA GGT CTC CTC AGG GTG GGG GGT
GGT GGG AGG TAC GAG GAG TGG ACA GAT CCA GAG GAG TCC CAC CCC CCA

      1930       1940       1950       1960       1970
        *          *          *          *          *
GAC AGT GCC TTC TCT ATT GGC ACA GCC TAG GGT CTT GGG GGT CAG GGG
CTG TCA CGG AAG AGA TAA CCG TGT CGG ATC CCA GAA CCC CCA GTC CCC

        1980       1990       2000       2010
          *          *          *          *
GGA GAA GTT CTT GAT TCA GCC AAA TGC AGG GAG GGG AGG CAG ATG GAG
CCT CTT CAA GAA CTA AGT CGG TTT ACG TCC CTC CCC TCC GTC TAC CTC
```

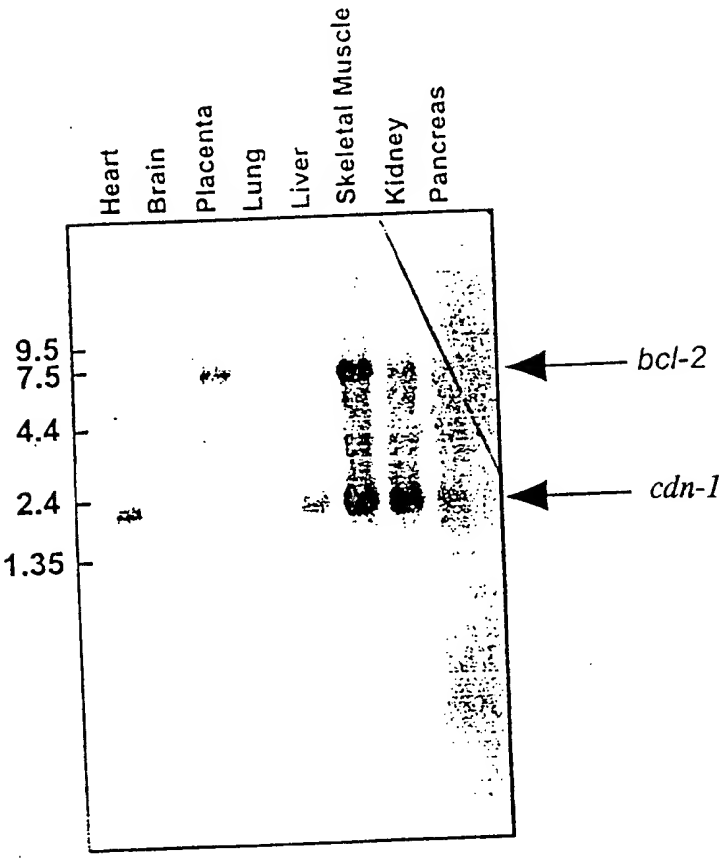
Figure 3 cont.

```
2020                2030                2040                2050                2060
 *                   *                   *                   *                   *
CCC ATA GGC CAC CCC CTA TCC TCT GAG TGT TTG GAA ATA AAC TGT GCA
GGG TAT CCG GTG GGG GAT AGG AGA CTC ACA AAC CTT TAT TTG ACA CGT

   2070                2080                2090
    *                   *                   *
ATC CCC TCA AAA AAA AAA CGG AGA TCC
TAG GGG AGT TTT TTT TTT GCC TCT AGG
```

Figure 4

Multiple Tissue Northern
bcl-2 and cdn-1 hybridization



Random primed. Klenow-labeled fragments of bcl-2 and cdn-1 clones were hybridized to a multiple human tissue Northern blot (Clontech 7760-1), at a final concentration of $1x10^6$ cpm/ml for each probe. Blot was washed at high stringency.

Figure 5 cdn-2 gene sequence

```
         10          20          30          40          50          60
          *           *           *           *           *           *
TTT TAA TAT AAA TTA ATG TGC TCT ATT TAT AGA GAC AAT ACA TGA AAT ATA CTT AAT AAA
AAA ATT ATA TTT AAT TAC ACG AGA TAA ATA TCT CTG TTA TGT ACT TTA TAT GAA TTA TTT

         70          80          90         100         110         120
          *           *           *           *           *           *
AAT TCA AAT GTT ATA GAA CTG AAA AAG ATG AAA AGT AAA AAC AAC CTA TTC CCC AGA GGT
TTA AGT TTA CAA TAT CTT GAC TTT TTC TAC TTT TCA TTT TTG TTG GAT AAG GGG TCT CCA

        130         140         150         160         170         180
          *           *           *           *           *           *
AGC CAC TGT CCA TAG TTT CTA TTT TAG ATT CTT TCC TTT ATA CAA GAT TAT TAT AGC TTC
TCG GTG ACA GGT ATC AAA GAT AAA ATC TAA GAA AGG AAA TAT GTT CTA ATA ATA TCG AAG

        190         200         210         220         230         240
          *           *           *           *           *           *
TAT TTT TTG GTG TAT GAA CTG TAG TCC TAG AGG ATT TTA TTA GTT ATG AGT TCT ATA ACT
ATA AAA AAC CAC ATA CTT GAC ATC AGG ATC TCC TAA AAT AAT CAA TAC TCA AGA TAT TGA

        250         260         270         280         290         300
          *           *           *           *           *           *
AAG ATC CAT CAT CTT AGT TGC TAA GAA CGT AGA TAC TGA GAA CAT CAT TTA AAA AAA CAT
TTC TAG GTA GTA GAA TCA ACG ATT CTT GCA TCT ATG ACT CTT GTA GTA AAT TTT TTT GTA

        310         320         330         340         350         360
          *           *           *           *           *           *
TTT TGG CTG GCA CCT CAT GAT CAC TGG AGT CTC GCG GGT CCC TCA GGC TGC ACA GGG ACA
AAA ACC GAC CGT GGA GTA CTA GTG ACC TCA GAG CGC CCA GGG AGT CCG ACG TGT CCC TGT

        370         380         390         400         410         420
          *           *           *           *           *           *
AGT AAA GGC TAC ATC CAG ATG CTG GGA ATG CAC TGA CGC CCA TTC CTG GAA ACT GGG CTC
TCA TTT CCG ATG TAG GTC TAC GAC CCT TAC GTG ACT GCG GGT AAG GAC CTT TGA CCC GAG

        430         440         450         460         470         480
          *           *           *           *           *           *
CCA CTC AGC CCC TGG GAG CAG CAG CCG CCA GCC CCT CGG GAC CTC CAT CTC CAC CCT GCT
GGT GAG TCG GGG ACC CTC GTC GTC GGC GGT CGG GGA GCC CTG GAG GTA GAG GTG GGA CGA

                        >BamHI
        490         500|        510         520         530         540
          *           *|          *           *           *           *
GAG CCA CCC GGG TTG GGC CAG GAT CCC GGC AGG CTG ATC CCG TCC TCC ACT GAG ACC TGA
CTC GGT GGG CCC AAC CCG GTC CTA GGG CCG TCC GAC TAG GGC AGG AGG TGA CTC TGG ACT

        550         560         570         580         590         600
          *           *           *           *           *           *
AAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC GGA GAG CCT GCC CTG
TTT TAC CGA AGC CCC GTT CCG GGT CCA GGA GGG TCC GTC CTC ACG CCT CTC GGA CGG GAC
     M   A   S   G   Q   G   P   G   P   P   R   Q   E   C   G   E   P   A   L>

        610         620         630         640         650         660
          *           *           *           *           *           *
CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC ACA GAG GAG GTT TTC CGC AGC TAC GTT
GGG AGA CGA AGA CTC CTC GTC CAT CGG GTC CTG TGT CTC CTC CAA AAG GCG TCG ATG CAA
 P   S   A   S   E   E   Q   V   A   Q   D   T   E   E   V   F   R   S   Y   V>

        670         680         690         700         710         720
          *           *           *           *           *           *
TTT TAC CAC CAT CAG CAG GAA CAG GAG GCT GAA GGG GCG GCT GCC CCT GCC GAC CCA GAG
AAA ATG GTG GTA GTC GTC CTT GTC CTC CGA CTT CCC CGC CGA CGG GGA CGG CTG GGT CTC
 F   Y   H   H   Q   Q   E   Q   E   A   E   G   A   A   P   A   D   P   E>
```

Figure 5 cont.

```
                                                    >Nco1
          730         740         750         760         770         780
            *           *           *           *           *           *
ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC GCC
TAC CAG TGG AAT GGA GAC GTT GGA TCG TCG TGG TAC CCC GTC CAC CCT GCC GTC GAG CGG
 M   V   T   L   P   L   Q   P   S   S   T   M   G   Q   V   G   R   Q   L   A>

          790         800         810         820         830         840
            *           *           *           *           *           *
ATC ATT GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG ACC ATG TTG CAG CAC
TAG TAA CCC CTG CTG TAG TTG GCT GCG ATA CTG AGT CTC AAG GTC TGG TAC AAC GTC GTG
 I   I   G   D   D   I   N   R   R   Y   D   S   E   F   Q   T   M   L   Q   H>

   >Pst1
     |    850         860         870         880         890         900
     |      *           *           *           *           *           *
CTG CAG CCC ACG GCA GAG AAT GCC TAT GAG TAC TTC ACC AAG ATT GCC TCC AGC CTG TTT
GAC GTC GGG TGC CGT CTC TTA CGG ATA CTC ATG AAG TGG TTC TAA CGG AGG TCG GAC AAA
 L   Q   P   T   A   E   N   A   Y   E   Y   F   T   K   I   A   S   S   L   F>

          910         920         930         940         950         960
            *           *           *           *           *           *
GAG AGT GGC ATC AAT TGG GGC CGT GTG GTG GCT CTT CTG GGC TTC AGC TAC CGT CTG GCC
CTC TCA CCG TAG TTA ACC CCG GCA CAC CAC CGA GAA GAC CCG AAG TCG ATG GCA GAC CGG
 E   S   G   I   N   W   G   R   V   V   A   L   L   G   F   S   Y   R   L   A>

          970         980         990         1000        1010        1020
            *           *           *           *           *           *
CTA CAC ATC TAC CAG CGT GGC CTG ACT GGC TTC CTG GGC CAG GTG ACC CGC TTT GTG GTG
GAT GTG TAG ATG GTC GCA CCG GAC TGA CCG AAG GAC CCG GTC CAC TGG GCG AAA CAC CAC
 L   H   I   Y   Q   R   G   L   T   G   F   L   G   Q   V   T   R   F   V   V>

          1030        1040        1050        1060        1070        1080
            *           *           *           *           *           *
GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG ATT GCA CAG AGG GGT GGC TGG GTG GCA
CTG AAG TAC GAC GTA GTG ACG TAA CGG GCC ACC TAA CGT GTC TCC CCA CCG ACC CAC CGT
 D   F   M   L   H   H   C   I   A   R   W   I   A   Q   R   G   G   W   V   A>

          1090        1100        1110        1120        1130        1140
            *           *           *           *           *           *
GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC GTG CTG GTG GTT CTG GGT GTG GTT CTG
CGG GAC TTG AAC CCG TTA CCA GGG TAG GAC TTG CAC GAC CAC CAA GAC CCA CAC CAA GAC
 A   L   N   L   G   N   G   P   I   L   N   V   L   V   V   L   G   V   V   L>

          1150        1160        1170        1180        1190        1200
            *           *           *           *           *           *
TTG GGC CAG TTT GTG GTA CGA AGA TTC TTC AAA TCA TGA CTC CCA AGG GTG CCT TTG GGG
AAC CCG GTC AAA CAC CAT GCT TCT AAG AAG TTT AGT ACT GAG GGT TCC CAC GGA AAC CCC
 L   G   Q   F   V   V   R   R   F   F   K   S   *>

          1210        1220        1230        1240        1250        1260
            *           *           *           *           *           *
TCC CAG TTC AGA CCC CTG CCT GGA CTT AAG CGA AGT CTT TGC CTT CTC TGC TCC TTG CAG
AGG GTC AAG TCT GGG GAC GGA CCT GAA TTC GCT TCA GAA ACG GAA GAG ACG AGG AAC GTC

                          >Hind3
          1270        1280    |
            *           *     |
GGT CCC CCC TCA AGA GTA CAG AAG CTT
CCA GGG GGG AGT TCT CAT GTC TTC GAA
```

Figure 6 Amino acid sequences of cdn-1, cdn-2, and bcl-2 family proteins

```
cdn1                                                                masgqgpgpprqecgepalpsaseeqvaqdteevfrsyvfyrhqqeqeaegvaapadpemvt
cdn2                                                                masgqgpgpprqecgepalpsaseeqvaqdteevfrsyvfyHhqqeqeaegAaapadpemvt
bcl2                                                    mahagrtgyDNREIVMKYIHYKLSQRGYEWdagdvgaappgaapapgifssqpghtphtaasrdpvartsplqtpaapgaa
bax                                                                 mdgsgeqprgggptsseqimktgalllqgfiqdragrmggeap
bcl-x                                                       msqSNRELVVDFLSYKLSQKGYSWsqfsdveenrteapegtesemetpsaingnpswhladspavngatghsssl
mcl-1                                           ...(+123 aa)eldgyepeplgkrpavlpllelvgesGnntstdgslpstpppaeeeedelyrqsleiisrylreqatgakdtk
A1                                                                                                  maeselmhihslaehylqyvlq
bhrf                                                                                  maystreillalcirdsrvhgngtlhpvlelaar
LMW5-HL                                                                                                megeeliyhniineilvgy
ced9      mtrctadnsltnpayrrrtmatgemkeflgikgteptdfginsdaqdlpspsrqastrrmsigesidgkindweeprlDIEGFVVDYFTHRIRQNGMEWfgapg

cdn1      lplqpsstmgQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIATSLFESGI-NWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHH
cdn2      lplqpsstmgQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGI-NWGRVVALLGFSYRLALHIYQRGLTGFLGQVTRFVVDFMLHH
bcl2      agpalspvppVVHLTLRQAGDDFSRRYRRDFAEMSRQLHLtpftargRFATVVEELFRDGV-NWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEY-LNR
bax       elaldpvpqdastkklseclkrigdeldsnmelqrmiaavdtdsprevFFRVAADMFSDGNFNWGRVVALFYFASKLVLKALCTKVPELIRTIMGWTLDF-LRE
bcl-x     darevipma-AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGV-NWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATY-LND
mcl-1     pmgrsgatsrkalETLRRVGDGVQRNHETVFQGMLRKLDIKNEDDVKSLSRVMIHVFSDGVTNWGRIVTLISFGAFVAKHLKTINQESCIEPLAESITD-VLVR
A1        vpafesapsqacrvlqrvafsvqkeveknlksylddfhvesidtariiFNQVMEKEFEDGIINWGRIVTIFAFGGVLLKKLpqeqialdvcaykqvssfvaefi
bhrf      etplrlspedtvvlryhvlleeiiernsetftetwnrfithtehvdldfnsvfleifhD-LINWGRICGFIVFSARMAKYCKDANn-HLESTVITTAYNF-SEG
LMW5-HL   ikyymndihelspyqqqikkiltyydeclnkqvtitfsltnaqeiktQFTGVVTELFKrgdpslgralawmawcmhacrtlccnqstpyyvvdlsvrgmleaM-
ced9      lpcgvqpehemmrvmgtifekkhaenfetfceqLlavprisfslyqdvvrtvgnaqtdqcpMSYGRLIGLISFGGFVAAKMmesvelqgqvrnlfvytslfIKT

cdn1      CIAR--WIA-QR-GGWVAALNLGngpilnvlvvlgvvllgqfvvrrffks
cdn2      CIAR--WIA-QR-GGWVAALNLGngpilnvlvvlgvvllgqfvvrrffks
bcl2      HLHT--WI--QDNGGWDAFVELYgpsmrplfdfswlslktllslalvgacitlgaylghk
bax       RLLG--WI--QDQGGWDGLLSYFgtptwqtvtifvagvltasltiwkkmg
bcl-x     HLEP--WI--QENGGWDTFVELYgnnaaaesrkgqerfnrwfltgmtvagvvllgslfsrk
mcl-1     TKRD--WLVKQ--RGWDGFVEFFhvedleggirnvllafagvagvgaglaylir
A1        MNNTGEWI-RQ-NGGWEdgfikkfepksgwltflqmtgqiwemlfllk
bhrf      -LDG--WIHQQ--GGWStliednipgsrrfswtlflagltlsllvicsylfisrgrh
LMW5-HL   KHNLLPWMISH--GGQEEFLAFslhsqiysvifnikyflskfcnhhflrscvqllrkcnli
ced9      -RIRNNWKE-H-NRSWDDFMTLgkqmkedyeraeaekvgrrkqnrrwsmigagvtagaigivgvvvcgrmmfslk
```

SEQUENCE IDENTITY:

cdn1/cdn2 = 97%

Sequence Range: 1 to 5408

Figure 7 cdn-3 enzyme annotated sequence

```
GAATTCTGCT AATTAGTTAA ACAACCTTGA ACAAGTTGTT TCACTTCTCT CAGTCTCAGC TTCTCACTCA AAAATGCTCA 80
ATAATTTGTA AGACTTCGCT AATAATCTAC GACTCTACAA GAGGCAATAG GGTACTGTGG ACAGAGAGCA GGCTTTGGAA 160
ACACACAAGA CTGGGTTTAG ATTCCTGCAC TCCAGGCAGT GTGTGACTTG GCCAAGCTTC TTCACTTCTC TAAAGGCCCA 240
TCTGTGTATC TGTACAGGAA TGAATGAATG ACTATGTGCA GGCAAGCTAT GCAAACTCCA GGTTAAAATA TTGCCTTGGG 320
TTTTTTACTA AATTGTTCAA GCCCATGACA TTCTAGCAGA AAAAGCCTAG TCTCTCTTTC TTAAGGTGAT TGTGTGCATG 400
TGTTTTCCAG GAACTCTATG GGTTTCTCAA CCCAAATTCA CCCTGCCCTT GACCAAATGG CTCACCAGCT TCACGGATGC 480
TGCTCTGATG ACACAGCCTG CAGTCAGCAT CTGCCCCTGC AGCTAGAATG CATTTCTGAG TGGGCATTAG CTGGGGGATA 560
GCACATGGGC ACCAATGTCA CAGATCTTCT GTCACAGTCC ACCCCCAACC ATTGCTTCTC AAATCATAAT CCCTTAGCAG 640
GACAGCTACG TGCAGCACGC ATGACACAAA CACCAGCCCT TGCCTACAAT CTCAGCCACT ATCTTGAGTC TGAGCAACTA 720
CTCTAGTGGC AGCCGGGCCC TTCCTTTTCA AGAGAGTTCT GGGATCAGAT CCTTTCACAA ACAGATGGCT CCCCAGCCTG 800
CCTGTTGTCC AGGTCTGCAC ACTGAAAAGT AAGACAGCAT TTGCTAAGCC ATATTTCAAA AAGTTTGCTT ATACCTTCAT 880
CTCAGGACAA CAAGTGCCTG CTTAAGAGCC TTATGTTTGT GTAACTGGTA TTTTTTTTTC CCCTGACCTT CCAAGGCCTA 960
GTCTACTTTC TGCCTCCCTA GCTGAAGAAA AGTCAACTTG AAATAATTTC AACTACCCCT TTTAGTGGGC AGCCCATTTG 1040
ATTTTTAGCT TAGCCAGAGC CTTAATTTGT GCATGTCAGC ATAGCAGTAC CTTCCAGCAC CTGAGGCACA ATACATTGTT 1120
TAAAGAGTGA CAGTGCGTCC CATTGCAATA AGAACCACAC TCAGAGCAAA GCTTCCCTCT CCTGTGTGGA GAGTGACCCA 1200
TGGTAGAAAA TTTGCAGACT TCCTTAGCTC TTCATCAGTT GAAAAATCTA TTTATTCATT TATGCATTTA ATTTTCCCTA 1280
TCTAAGCCAG CGATAGTCAA ACATTTTCTG TAAAGGGCCA AGCAGCATGA TAAATATGTT AGGCTCTGCA GGCCACTTAC 1360
AGTTTTGTCA TGTATTCTTT TTTTGCTGGC TGTTTGTATT ATTTTGTTTA CAATGCTTTA AAAATCTAAA AAAACAGATG 1440
ATCACTGGAG TCTCAGGGCT CCCTGGGGCC ACACAGGGAC AAGCAAAGGC TACATGCAGA TACCAGAAAT GCACTGACGC 1520
CCGTTCCTGG AAGCTGGGCT CCCACTCAGC CCCTGGGAGC AGCAGCCTCC AGCCCCTTGG GACCTTCAAC TGGAGCCTGC 1600
```

Figure 7 cont.

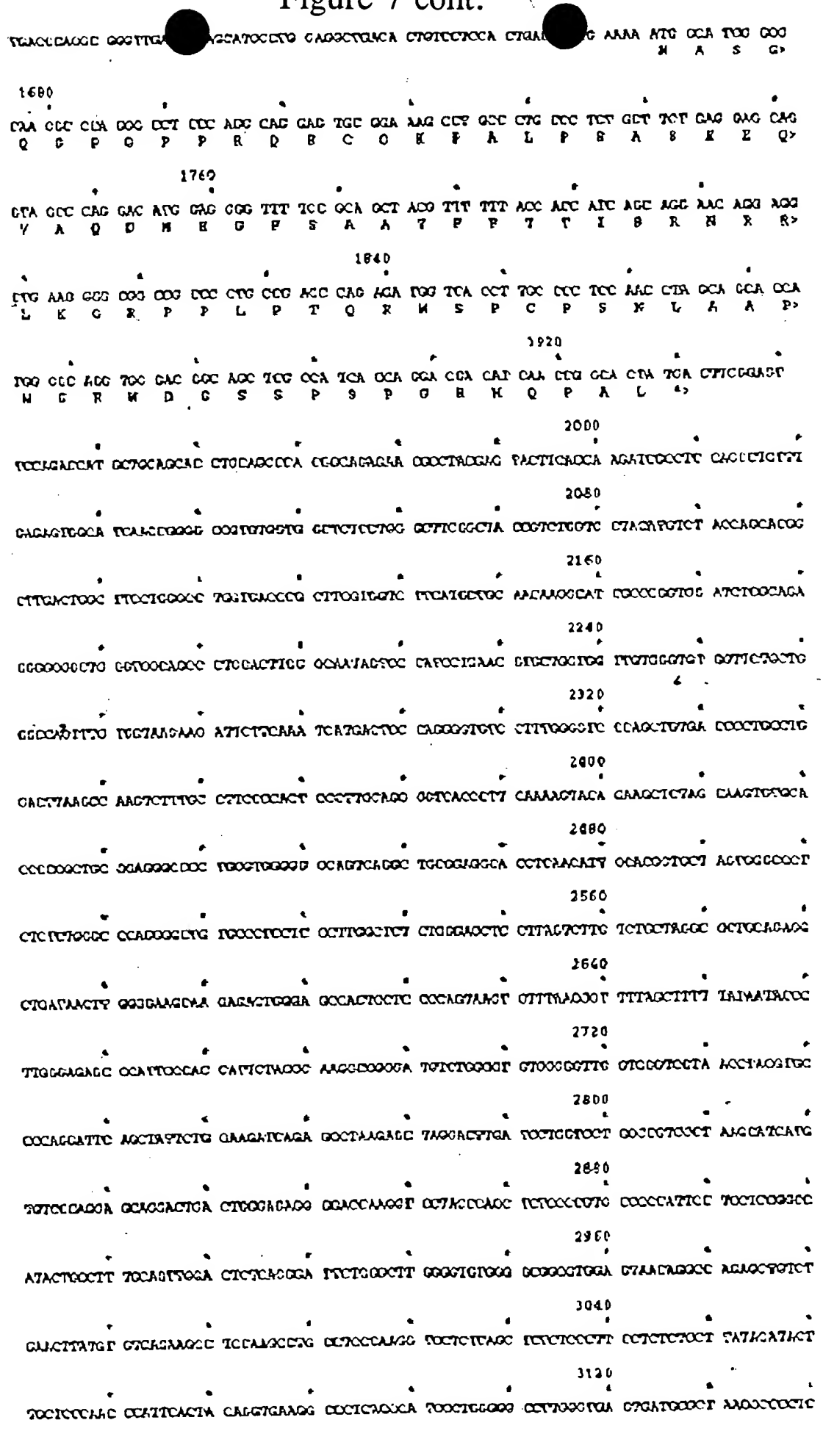


Figure 7 cont.

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                                                              00
CCCGCCCAGA CTACAGGGCT TGGTTTAGGG CTTGGTTTGT TATTTCAGGG ATAAGGAGTA GGGAGTTCAT CTGGAAGGTT
                                                              3280
CTAACTGGGA CAAGGACTAT CAAGAGCACA GGAAATCCAG AGGTGGGATC CTCCCTCATG GCTCTGGCAC AGTGTAATCC
                                                              3360
AGGGGTGGAG ATAGGGAACT GTGAATAGCT GAACTCTGTC GGGGGACGCT CCATGCTCCT CACCTTTCTG GCTCTCTGCT
                                                              3440
CAGTGTGGGG GTGAGAGTAC CTTCTCTATC GGGCACAGCC TAGGCTGTTG GGGGTGAAGG GGGAGAAGTT CTGGATTCAG
                                                              3520
CCAAATGCAG GGAGGGGAGG CAGAAGGAGC CCACAGGGCA CTCCCGATCC TCTGAGTGTT TGGAAATAAA CTGTGCAATC
                                                              3600
CCATCAAAAA AAAAAAGGAG AAAAAAATGT AAAAAACATG CTTAGCTGTA AGCTACTTAT AGGGGCATAA AGACAGGACT
                                                              3680
GTTAATGCAC ACAAACATAC ACTTAGAGAG AAGAAATAAG TTCTGTGCAG GCACGGTGCC TCACAGCTCT AACTCCAGCA
                                                              3760
CTTTGGGAGA GCAAAGTGGG AAGATCATTT GAGTCCAGGA GTTGGAGACC AGCCTGGACA ACATAGCAAG ATCTTATCTC
                                                              3840
TACAGAAAAT TTAAAAAAAA GAAAAAAACT AGGCGCACAG GTCTGCAGTC CTAGCTACTC CGGAGGCTAA GGTGGGAGAA
                                                              3920
TCCTTGAACC CAGGGATTTA GTTTGAGCTT GCAGTGAGCT ATGATTGCAC CACTGCACTC CAGACTGGGT GACTGAGTCA
                                                              4000
GACCCTGTCT CAAATATAAA GAAGAAACAA GTTCTAGTTT TCAATAGGGC AATAGGGTGA GTGCAGTTAG CAACAACATA
                                                              4080
TTGTGTATTT CAAAATAGCT ACAAGAGAGG ATATGAAGTG TTGCTCCAAA CAAGGAATGA TAAGGTTGGA GGTGACAGAT
                                                              4160
ACCTTAAATA CCCTGATTTG ATCATTACAC ATTCAATGTA TGTATCAAAA CATTACATGT ACCCCACAAA TTTGTGTAAA
                                                              4240
TATTATGTAT CCACTTTTTA AAGTTGGCAG ACCCCAAAAC CACTACTATG GCTTCCAGTG GTCACTGTGA GCACTGCCAG
                                                              4320
CTCAGCAAAT GTATCACCCA AAATCTGGGC AATGTGGGAA ATTGGCTTCA TGGCAGCTAT GGCTTTGGCA CTGATAGGAA
                                                              4400
TGATTTCCAG AGATACTTAA TCCTCAATTC GGGACTCTTT GCTTCAGGAG TTTGGCTGGC CAGGAACATG AGTGACAGTG
                                                              4480
AGCTCTTGGC ACTTCAGCTG GGGGTGTAGC CAAGCAGACA AATGGAATCT TGTGCTGAAC CCAAACCTTC TAGAAACAGA
                                                              4560
GGCTGTCAGC ATCACAAGAT ATGGGCTGAT GGAAGCTGAA GTTTAATTCA GCTGAGCCCT TGCCCCTTTC CAACCTGGTT
                                                              4640
TCTTTTAGTT CCTTGAGTCC AGTCAGAATG GCATTCCCTG GCCAGCAGGC AGCCTTTAGT CACTGTCTCT GTTCTGCAAA
                                                              4720
GCTCTGTATA TAGTTACTGA GTTTCTGCAG GGGCTGATCT TTGCTCTTGT CCTAAGAAAT AACTACAGTG TTTTAAGAAA
                                                              4800
TATTTGAGGC GGGCTGCAGT GGTTCACACC TGTAATGCAG CACTTTGGGA GGCCAAGGCA GGTGGATCAT GAGGTCAAGA
```

Figure 7 cont.

```
                                                                  4880
GTTTCAGACC ATCATGGCCA ACATGGTGAA ACCCCATCTC TACTAAAAAT ACAAAAATTA GCTGGGTGTG GTGGCGGGCA

                                                                  4960
GCTGTAGTCC CAGCTACTCG GGAGGCTGAG GCAGGAGAAT GGCTTGAGCC TGGGAGGCGG AGGTTGCAGT GAGCCGAGAT

                                                                  5040
CACGCCACTG CACTCCAGCC TGGGCGACAGA GCGAGACTCC ATCTCAAAAA AAAGAAAAAA TAAATAGTTG AAATAAAGAC

                                                                  5120
TGCACATAAA GACAAAAAAA AAGTTTATAA AGTTAAAAAA TAAAATAAAA AACAGGCTCC AGGCTGGATT GGGCCCAGAG

                                                                  5200
GCTGTAGGAC ACAGACCCCC AGGCAATGAC TTCATAAATC CCGATGTTAA TCACCCTCAC CTGGGAATTT GGGGAGGGGA

                                                                  5280
CTCATTTTAA AACAGTTTCC TGGATTCTAA CCCAACCCAG AAAATCAGAC TCTTTGAGCT AAATTCTTAA GCTCCCTGGT

                                                                  5360
GATGATGATG GAAGCAGTTT ATGGCTCACC CCAGAGTAGC GTCTGAAAGA CCTCCCACAT CCCTCTCTCT CCAGCCTCCC

CTTCTCCTCC ATTCCCCAGC GAGAATTC
```

Figure 8

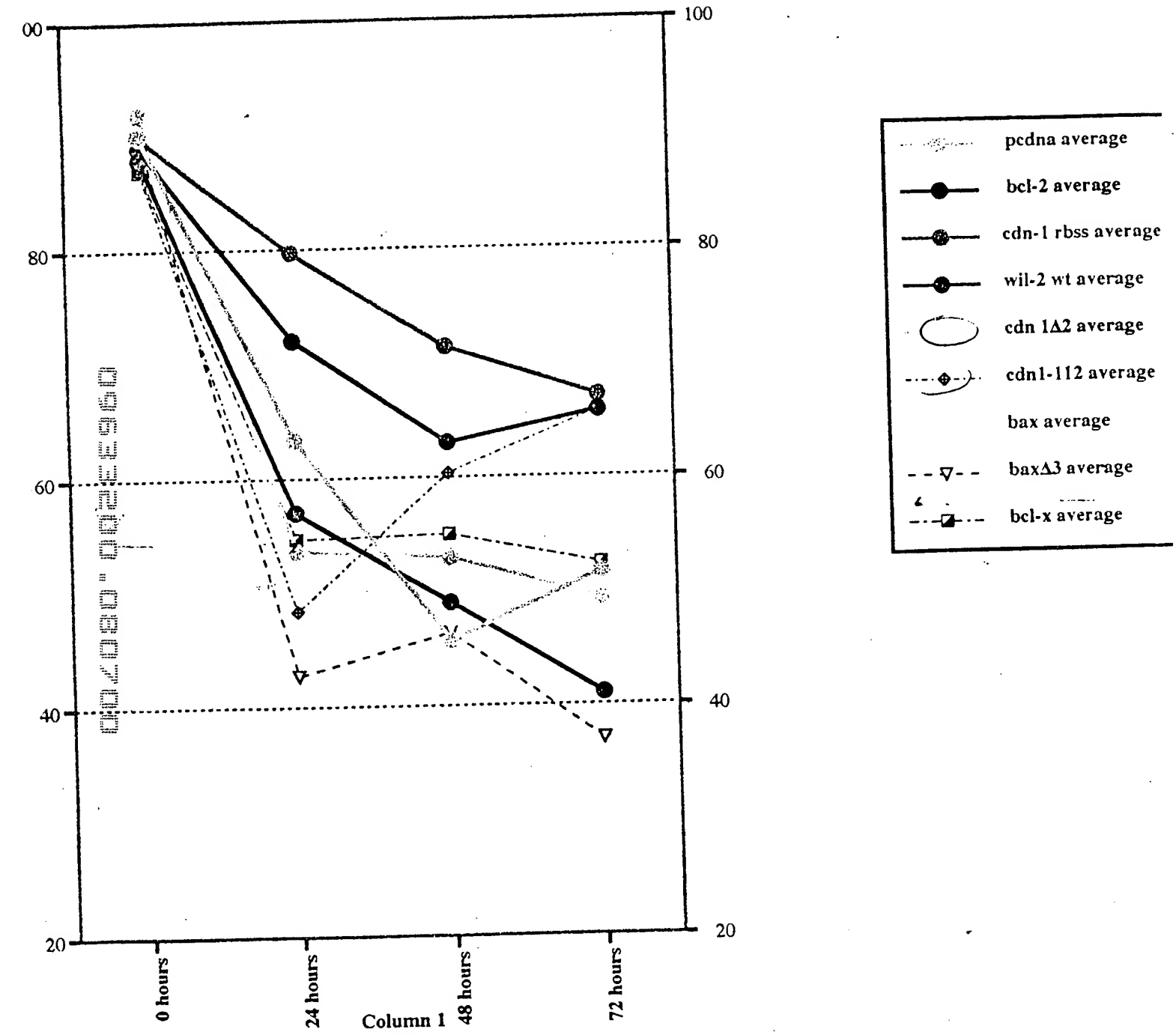
Wil-2 transformants 0.1% FBS
00
80
60
40
20
100
80
60
40
20
0 hours
24 hours
48 hours
72 hours
Column 1
pcdna average
bcl-2 average
cdn-1 rbss average
wil-2 wt average
cdn 1Δ2 average
cdn1-112 average
bax average
baxΔ3 average
bcl-x average

Figure 9

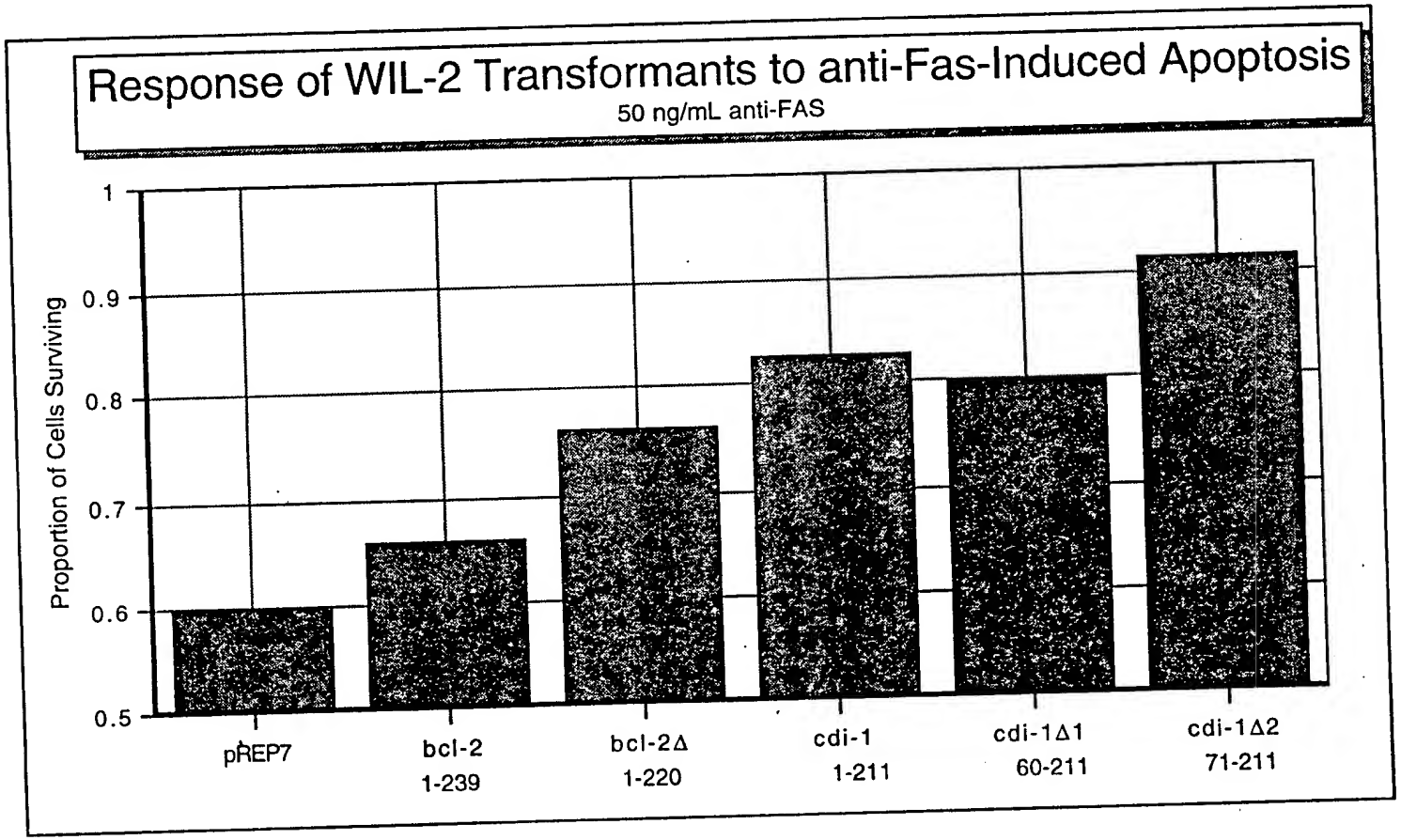
Response of WIL-2 Transformants to anti-Fas-Induced Apoptosis
50 ng/mL anti-FAS
Proportion of Cells Surviving
1
0.9
0.8
0.7
0.6
0.5
pREP7
bcl-2
1-239
bcl-2Δ
1-220
cdi-1
1-211
cdi-1Δ1
60-211
cdi-1Δ2
71-211

Figure 10

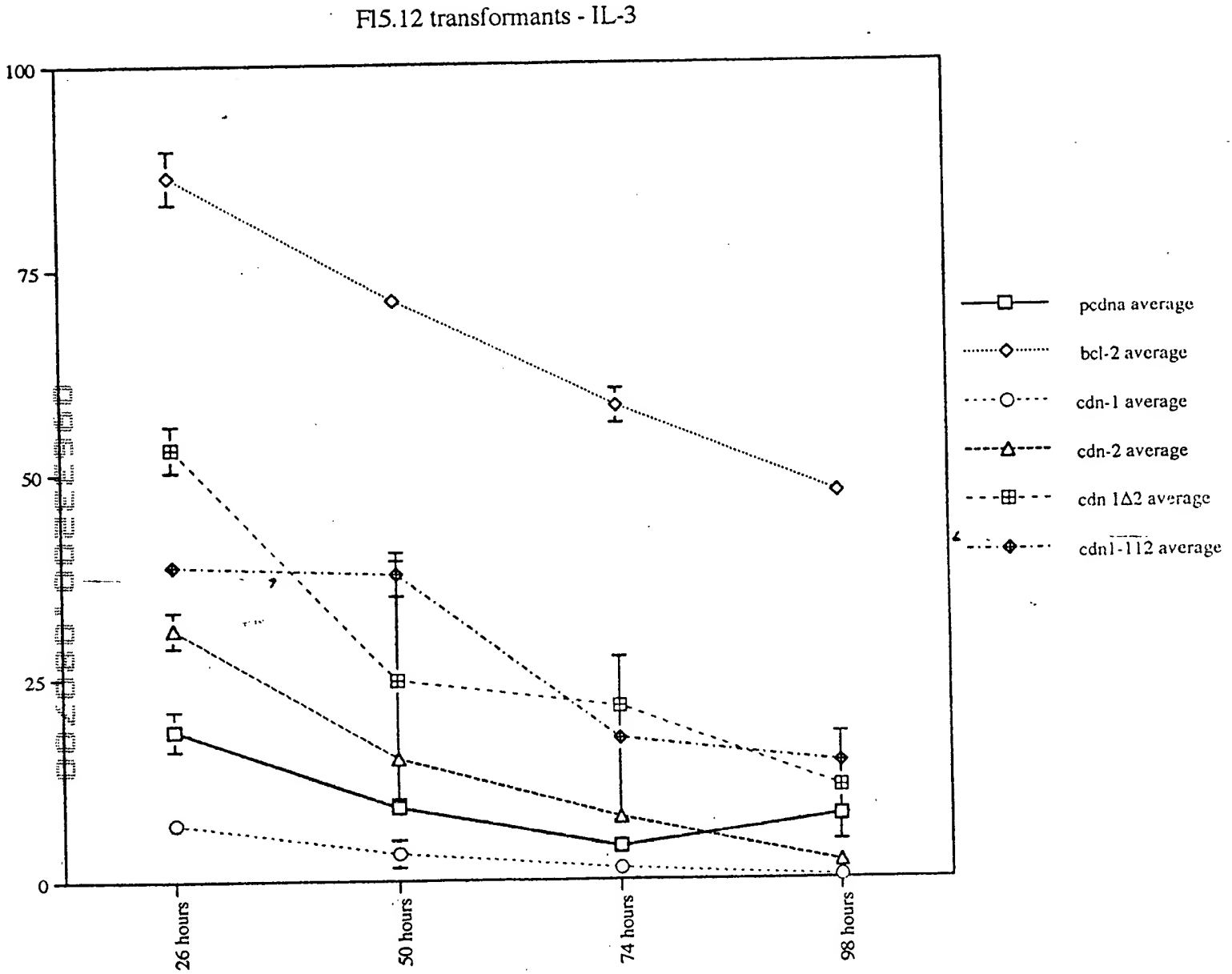
Fl5.12 transformants - IL-3
100
75
50
25
0
26 hours
50 hours
74 hours
98 hours
pcdna average
bcl-2 average
cdn-1 average
cdn-2 average
cdn 1Δ2 average
cdn1-112 average

Figure 11 N-terminal methionine residues of cdn-1 derivatives